

#12 1652

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1600

RAW SEQUENCE LISTING

DATE: 11/13/2002

PATENT APPLICATION: US/09/701,586C

TIME: 15:44:32

Input Set : A:\701586sq

Output Set: N:\CRF4\11132002\I701586C.raw

3 <110> APPLICANT: Kock, Michael
 4 Hoeger, Thomas
 5 Kroeger, Burkhard
 6 Otterbach, Bernd
 7 Lubisch, Wilfried
 8 Lemaire, Hans-Georg
 10 <120> TITLE OF INVENTION: Poly (ADP-ribose) polymerase-gene
 12 <130> FILE REFERENCE: 0050/49100
 14 <140> CURRENT APPLICATION NUMBER: US 09/701,586C
 C--> 15 <141> CURRENT FILING DATE: 2000-11-30
 17 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03889
 18 <151> PRIOR FILING DATE: 1999-06-04
 20 <160> NUMBER OF SEQ ID NOS: 33
 22 <170> SOFTWARE: PatentIn/WordPerfect
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1843
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (3)...(1715)
 32 <223> OTHER INFORMATION: product is Poly ADP Ribose Polymerase; from brain tissue
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 37 Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg
 38 1 5 10 15
 40 gca tta aat gaa agc aaa aga gtt aat aat ggc aac acg gct cca gaa 95
 41 Ala Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu
 42 20 25 30
 44 gac tct tcc cct gcc aag aaa act cgt aga tgc cag aga cag gag tgc 143
 45 Asp Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser
 46 35 40 45
 48 aaa aag atg cct gtg gct gga gga aaa gct aat aag gac agg aca gaa 191
 49 Lys Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu
 50 50 55 60
 52 gac aag caa gat gaa tct gtg aag gcc ttg ctg tta aag ggc aaa gct 239
 53 Asp Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Lys Gly Lys Ala
 54 65 70 75
 56 cct gtg gac cca gag tgt aca gcc aag gtg ggg aag gct cat gtg tat 287
 57 Pro Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr
 58 80 85 90 95
 60 tgt gaa gga aat gat gtc tat gat gtc atg cta aat cag acc aat ctc 335
 61 Cys Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu

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62	100	105	110	
64	cag ttc aac aac aac aag tac tat ctg att cag cta tta gaa gat gat	383		
65	Gln Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp			
66	115 120 125			
68	gcc cag agg aac ttc agt gtt tgg atg aga tgg ggc cga gtt ggg aaa	431		
69	Ala Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys			
70	130 135 140			
72	atg gga cag cac agc ctg gtg gct tgt tca ggc aat ctc aac aag gcc	479		
73	Met Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala			
74	145 150 155			
76	aag gaa atc ttt cag aag aaa ttc ctt gac aaa acg aaa aac aat tgg	527		
77	Lys Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp			
78	160 165 170 175			
80	gaa gat cga gaa aag ttt gag aag gtg cct gga aaa tat gat atg cta	575		
81	Glu Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu			
82	180 185 190			
84	cag atg gac tat gcc acc aat act cag gat gaa gag gaa aca aag aaa	623		
85	Gln Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys			
86	195 200 205			
88	gag gaa tct ctt aaa tct ccc ttg aag cca gag tca cag cta gat ctt	671		
89	Glu Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu			
90	210 215 220			
92	cgg gta cag gag tta ata aag ttg atc tgt aat gtt cag gcc atg gaa	719		
93	Arg Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu			
94	225 230 235			
96	gaa atg atg atg gaa atg aag tat aat acc aag aaa gcc cca ctt ggg	767		
97	Glu Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly			
98	240 245 250 255			
100	aag ctg aca gtg gca caa atc aag gca ggt tac cag tct ctt aag aag	815		
101	Lys Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys			
102	260 265 270			
104	att gag gat tgt att cgg gct ggc cag cat gga cga gct ctc atg gaa	863		
105	Ile Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu			
106	275 280 285			
108	gca tgc aat gaa ttc tac acc agg att ccg cat gac ttt gga ctc cgt	911		
109	Ala Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg			
110	290 295 300			
112	act cct cca cta atc cgg aca cag aag gaa ctg tca gaa aaa ata caa	959		
113	Thr Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln			
114	305 310 315			
116	tta cta gag gct ttg gga gac att gaa att gct att aag ctg gtg aaa	1007		
117	Leu Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys			
118	320 325 330 335			
120	aca gag cta caa agc cca gaa cac cca ttg gac caa cac tat aga aac	1055		
121	Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn			
122	340 345 350			
124	cta cat tgt gcc ttg cgc ccc ctt gac cat gaa agt tac gag ttc aaa	1103		
125	Leu His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys			
126	355 360 365			

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128 gtg att tcc cag tac cta caa tct acc cat gct ccc aca cac agc gac      1151
129 Val Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp
130      370      375      380
132 tat acc atg acc ttg ctg gat ttg ttt gaa gtg gag aag gat ggt gag      1199
133 Tyr Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu
134      385      390      395
136 aaa gaa gcc ttc aga gag gac ctt cat aac agg atg ctt cta tgg cat      1247
137 Lys Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His
138 400      405      410      415
140 ggt tcc agg atg agt aac tgg gtg gga atc ttg agc cat ggg ctt cga      1295
141 Gly Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg
142      420      425      430
144 att gcc cca cct gaa gct ccc atc aca ggt tac atg ttt ggg aaa gga      1343
145 Ile Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly
146      435      440      445
148 atc tac ttt gct gac atg tct tcc aag agt gcc aat tac tgc ttt gcc      1391
149 Ile Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala
150      450      455      460
152 tct cgc cta aag aat aca gga ctg ctg ctc tta tca gag gta gct cta      1439
153 Ser Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu
154      465      470      475
156 ggt cag tgt aat gaa cta cta gag gcc aat cct aag gcc gaa gga ttg      1487
157 Gly Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu
158 480      485      490      495
160 ctt caa ggt aaa cat agc acc aag ggg ctg ggc aag atg gct ccc agt      1535
161 Leu Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser
162      500      505      510
164 tct gcc cac ttc gtc acc ctg aat ggg agt aca gtg cca tta gga cca      1583
165 Ser Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro
166      515      520      525
168 gca agt gac aca gga att ctg aat cca gat ggt tat acc ctc aac tac      1631
169 Ala Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr
170      530      535      540
172 aat gaa tat att gta tat aac ccc aac cag gtc cgt atg cgg tac ctt      1679
173 Asn Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu
174      545      550      555
176 tta aag gtt cag ttt aat ttc ctt cag ctg tgg tga atgttgatat      1725
177 Leu Lys Val Gln Phe Asn Phe Leu Gln Leu Trp
178 560      565      570
180 taaataaacc agagatctga tcttcaagca agaaaataag cagtgttgta cttgtgaatt      1785
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186 <211> LENGTH: 570
187 <212> TYPE: PRT
188 <213> ORGANISM: Homo sapiens
190 <400> SEQUENCE: 2
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193 1      5      10      15
195 Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu Asp

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196		20		25		30	
198	Ser	Ser	Pro	Ala	Lys	Lys	Thr
199		35		40		45	
201	Lys	Met	Pro	Val	Ala	Gly	Gly
202		50		55		60	
204	Lys	Gln	Asp	Glu	Ser	Val	Lys
205	65			70		75	
207	Val	Asp	Pro	Glu	Cys	Thr	Ala
208			85			90	
210	Glu	Gly	Asn	Asp	Val	Tyr	Asp
211			100			105	
213	Phe	Asn	Asn	Asn	Lys	Tyr	Tyr
214			115			120	
216	Gln	Arg	Asn	Phe	Ser	Val	Trp
217		130				135	
219	Gly	Gln	His	Ser	Leu	Val	Ala
220	145					150	
222	Glu	Ile	Phe	Gln	Lys	Lys	Phe
223				165		170	
225	Asp	Arg	Glu	Lys	Phe	Glu	Lys
226			180			185	
228	Met	Asp	Tyr	Ala	Thr	Asn	Thr
229		195				200	
231	Glu	Ser	Leu	Lys	Ser	Pro	Leu
232		210				215	
234	Val	Gln	Glu	Leu	Ile	Lys	Leu
235	225					230	
237	Met	Met	Met	Glu	Met	Lys	Tyr
238				245		250	
240	Leu	Thr	Val	Ala	Gln	Ile	Lys
241			260			265	
243	Glu	Asp	Cys	Ile	Arg	Ala	Gly
244			275			280	
246	Cys	Asn	Glu	Phe	Tyr	Thr	Arg
247		290				295	
249	Pro	Pro	Leu	Ile	Arg	Thr	Gln
250	305					310	
252	Leu	Glu	Ala	Leu	Gly	Asp	Ile
253				325		330	
255	Glu	Leu	Gln	Ser	Pro	Glu	His
256			340			345	
258	His	Cys	Ala	Leu	Arg	Pro	Leu
259			355			360	
261	Ile	Ser	Gln	Tyr	Leu	Gln	Ser
262		370				375	
264	Thr	Met	Thr	Leu	Leu	Asp	Leu
265	385					390	
267	Glu	Ala	Phe	Arg	Glu	Asp	Leu
268				405		410	

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Input Set : A:\701586sq

Output Set: N:\CRF4\11132002\I701586C.raw

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270 Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg Ile
271          420          425          430
273 Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly Ile
274          435          440          445
276 Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala Ser
277          450          455          460
279 Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu Gly
280 465          470          475          480
282 Gln Cys Asn Glu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu Leu
283          485          490          495
285 Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser Ser
286          500          505          510
288 Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro Ala
289          515          520          525
291 Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr Asn
292          530          535          540
294 Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu Leu
295 545          550          555          560
297 Lys Val Gln Phe Asn Phe Leu Gln Leu Trp
298          565          570
301 <210> SEQ ID NO: 3
302 <211> LENGTH: 2265
303 <212> TYPE: DNA
304 <213> ORGANISM: Homo sapiens
306 <220> FEATURE:
307 <221> NAME/KEY: CDS
308 <222> LOCATION: (242)...(1843)
309 <223> OTHER INFORMATION: product is Poly ADP Ribose Polymerase; from uterus tissue
311 <400> SEQUENCE: 3
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315 tagccgatgt ctaatcccc acacaagctc atccccggcc tctgggattg ttgggaattc      120
317 tctccctaata tcacgctga ggctcatgga gagttgctag acctgggact gccctgggag      180
319 gcgcacacaa ccaggccggg tggcagccag gacctctccc atgtccctgc ttttcttggc      240
321 c atg gct cca aag ccg aag ccc tgg gta cag act gag ggc cct gag      286
322 Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu
323 1          5          10          15
325 aag aag aag ggc cgg cag gca gga agg gag gag gac ccc ttc cgc tcc      334
326 Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser
327          20          25          30
329 acc gct gag gcc ctc aag gcc ata ccc gca gag aag cgc ata atc cgc      382
330 Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg
331          35          40          45
333 gtg gat cca aca tgt cca ctc agc agc aac ccc ggg acc cag gtg tat      430
334 Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr
335          50          55          60
337 gag gac tac aac tgc acc ctg aac cag acc aac atc gag aac aac aac      478
338 Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn
339          65          70          75
341 aac aag ttc tac atc atc cag ctg ctc caa gac agc aac cgc ttc ttc      526

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/701,586C

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Input Set : A:\701586sq
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 2,3,4,5,6,7,9,10,11
Seq#:12; Xaa Pos. 1,2,6,7,9,10,11,12,13,14,16,17,18
Seq#:13; Xaa Pos. 6,7,8,9,10,11,12,13,16,17,21,22,24,25,26,27,28,29,31,32
Seq#:13; Xaa Pos. 33,41,42,43,48
Seq#:14; Xaa Pos. 1,2,3,4,5,6,7,9,10,11,12,13,14,16,17,18,19,20,21
Seq#:15; Xaa Pos. 2,3,4,5,6,7,8,9,10,12,13,15,16,20,21,22,23,24,25,26,27,28
Seq#:15; Xaa Pos. 29,30,31,32
Seq#:16; Xaa Pos. 2,3,4,6,8,9,10,11,14,16,18,19,20,21,22,24,25,26,28
Seq#:17; Xaa Pos. 2,4,5,6,8,9,10,11,12,13,14,15,16,18,19,20,21,22,23,24,25
Seq#:17; Xaa Pos. 26,27,33,34,35,38,39,40,41,42,43
Seq#:18; Xaa Pos. 4,8,11,12,13
Seq#:19; Xaa Pos. 2,3,4,6,7,9,13,15,16
Seq#:20; Xaa Pos. 2,3,4,6
Seq#:21; Xaa Pos. 2,3,5,6,7,8,10,11,12,14,15,16,17,18,19,20,21,22,24,26,27
Seq#:22; Xaa Pos. 2,3,4,6,7,8,10,11,12,13
Seq#:29; Xaa Pos. 2,3,4
Seq#:30; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23
Seq#:30; Xaa Pos. 24,25,26,27,28,29,30,31,32,33,34,36,37